SEQUENCE LISTING

<110> Abbott Laboratories
Mukerji, Pradip
Huang, Yung-Sheng
Pereira, Suzette L.

<120> DESATURASE GENES, ENZYMES ENCODED
THEREBY, AND USES THEREOF

<130> 6884.US.01

<140> 10/060,793
<141> 2002-01-30

<160> 60

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1144

<400> 1
atccgcgccg ccatccccaa gcactgctgg gtcaag 36

<210> 2
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1119

<221> misc_feature
<222> (21)...(21)
<223> y = t/u or c at position 21

<221> misc_feature
<222> (33)...(33)
<223> y = t/u or c at position 33

<400> 2
gccctcttcg tcctcggcca ygactgcggc cayggctcgt tctcg 45

<210> 3
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1118

<221> misc_feature
<222> (4)...(4)
<223> r = g or a at position 4

<221> misc_feature
<222> (10)...(10)
<223> r = g or a at position 10

<221> misc_feature
<222> (30)...(31)
<223> r = g or a at positions 30-31

<221> misc_feature
<222> (34)...(34)
<223> r = g or a at position 34

<221> misc_feature
<222> (38)...(38)
<223> r = g or a at poisition 38

<221> misc_feature
<222> (39)...(39)
<223> y = t/u or c at position 39

<221> misc_feature
<222> (43)...(43)
<223> r = g or a at position 43

<400> 3
gagrtggtar tgggggatct gggggaagar rtgrtggryg acrtg 45

<210> 4
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1121

<221> misc_feature
<222> (9)...(9)
<223> y = t/u or c at position 9

<221> misc_feature
<222> (27)...(27)
<223> y = t/u or c at position 27

<221> misc_feature
<222> (36)...(36)
<223> y = t/u or c at position 36

<221> misc_feature
<222> (39)...(39)
<223> y = t/u or c at position 39

<400> 4

ccctaccayg gctggcgcat ctcgcaycgc acccaycayc agaac 45

<210> 5
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1122

<221> misc_feature
<222> (7)...(7)
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<221> misc_feature
<222> (10)...(10)
<223> r = g or a at position 10

<221> misc_feature
<222> (37)...(37)
<223> r = g or a at position 37

<400> 5
gttctgrtgr tgggtccgrt gcgagatgcg ccagccrtgg taggg 45

<210> 6
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1146

<221> misc_feature
<222> (13)...(13)
<223> s = g or c at position 13

<221> misc_feature
<222> (19)...(19)
<223> k = g or t/u at position 19

<400> 6
ggctcgcact tcsaccccka ctcggacctc ttcgtc 36

<210> 7
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1147

<221> misc_feature
<222> (18)...(18)
<223> m = a or c at position 18

<221> misc_feature

<222> (24)...(24)
<223> w = a or t/u at position 24

<400> 7
gacgaagagg tccgagtmgg ggtwgaagtg cgagcc 36

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1148

<221> misc_feature
<222> (9)...(9)
<223> k = g or t/u at position 9

<221> misc_feature
<222> (30)...(30)
<223> w = a or t/u at position 30

<221> misc_feature
<222> (32)...(32)
<223> s = g or c at position 32

<400> 8
gcgctggakg gtggtgaggc cgccgcggaw gsacgacca 39

<210> 9
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1114

<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

<221> misc_feature
<222> (16)...(16)
<223> r = g or a at position 16

<221> misc_feature
<222> (25)...(25)
<223> r = g or a at position 25

<221> misc_feature
<222> (40)...(40)
<223> r = g or a at position 40

<221> misc_feature
<222> (43)...(43)
<223> r = g or a at position 43

<400> 9
ctgggggaag agrtgrtgga tgacrtgggt gccgatgtcr tgrtg 45

<210> 10
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1116

<221> misc_feature
<222> (12)...(12)
<223> y = t/u or c at position 12

<221> misc_feature
<222> (16)...(16)
<223> r = g or a at position 16

<221> misc_feature
<222> (22)...(22)
<223> r = g or a at position 22

<221> misc_feature
<222> (33)...(33)
<223> k = g or t/u at position 33

<221> misc_feature
<222> (42)...(43)
<223> r = g or at at positions 42-43

<400> 10
ggtggcctcg aygagrtggt artgggggat ctkggggaag arrtg 45

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1118

<221> misc_feature
<222> (4)...(4)
<223> r = g or a at position 4

<221> misc_feature
<222> (10)...(10)
<223> r = g or a at position 10

<221> misc_feature
<222> (30)...(31)
<223> r = g or a at positions 30-31

<221> misc_feature
<222> (34)...(34)
<223> r = g or a at position 34

<221> misc_feature
<222> (38)...(38)
<223> r = g or a at position 38

<221> misc_feature
<222> (39)...(39)
<223> y = t/u or c at position 39

<221> misc_feature
<222> (43)...(43)
<223> r = g or a at position 43

<400> 11
gagrtggtar tgggggatct gggggaagar rtgrtggryg acrtg 45

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1188

<400> 12
tacgcgtacc tcacgtactc gctcg 25

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1189

<400> 13
ttcttgcacc acaacgacga agcgacg 27

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1190

<400> 14
ggagtggacg tacgtcaagg gcaac 25

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1191

<400> 15
tcaagggcaa cctctcgagc gtcgac 26

<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO898

<400> 16
cccagtcacg acgttgtaaa acgacggcca g 31

<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO899

<400> 17
agcggataac aatttcacac aggaaacagc 30

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1185

<400> 18
ggtaaaagat ctcgtccttg tcgatgttgc 30

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1186

<400> 19
gtcaaagtgg ctcatcgtgc 20

<210> 20
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1187

<400> 20
cgagcgagta cgtgaggtac gcgtac 26

<210> 21
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1212

<400> 21
tcaacagaat tcatgaccga ggataagacg aaggtcgagt tcccg 45

<210> 22
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1213

<400> 22
aaaagaaagc ttcgcttcct agtcttagtc cgacttggcc ttggc 45

<210> 23
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1221

<400> 23
tcaacaaagc ttatgaccga ggataagacg aaggtcgagt tcccg 45

<210> 24
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1222

<400> 24
aaaagagaat tccgcttcct agtcttagtc cgacttggcc ttggc 45

<210> 25
<211> 1077
<212> DNA
<213> Saprolegnia diclina

<400> 25
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ccgaacgcgt gctttgagtc gaacctcggc ctctcgctct actacacggc ccgcgcgatc 120
ttcaacgcgt cggcctcggc ggcgctgctc tacgcggcgc gctcgacgcc gttcattgcc 180
gataacgttc tgctccacgc gctcgtttgc gccacctaca tctacgtgca gggcgtcatc 240
ttctggggct tcttcacggt cggccacgac tgcggccact cggccttctc gcgctaccac 300
agcgtcaact ttatcatcgg ctgcatcatg cactctgcga ttttgacgcc gttcgagagc 360

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tggcgcgtga cgcaccgcca ccaccacaag aacacgggca acattgataa ggacgagatc     420
ttttacccgc accggtcggt caaggacctc caggacgtgc gccaatgggt ctacacgctc     480
ggcggtgcgt ggtttgtcta cttgaaggtc gggtatgccc cgcgcacgat gagccacttt     540
gacccgtggg acccgctcct ccttcgccgc gcgtcggccg tcatcgtgtc gctcggcgtc     600
tgggccgcct tcttcgccgc gtacgcgtac ctcacatact cgctcggctt tgccgtcatg     660
ggcctctact actatgcgcc gctctttgtc tttgcttcgt tcctcgtcat tacgaccttc     720
ttgcaccaca acgacgaagc gacgccgtgg tacggcgact cggagtggac gtacgtcaag     780
ggcaacctct cgagcgtcga ccgctcgtac ggcgcgttcg tggacaacct gagccaccac     840
attggcacgc accaggtcca ccacttgttc ccgatcattc cgcactacaa gctcaacgaa     900
gccaccaagc actttgcggc cgcgtacccg cacctcgtgc gcaggaacga cgagcccatc     960
atcacggcct tcttcaagac cgcgcacctc tttgtcaact acggcgctgt gcccgagacg    1020
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<210> 26
<211> 358
<212> PRT
<213> Saprolegnia diclina

<400> 26

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Lys His Ser Ile Pro Asn Ala Cys Phe Glu Ser Asn Leu Gly Leu Ser
            20                  25                  30
Leu Tyr Tyr Thr Ala Arg Ala Ile Phe Asn Ala Ser Ala Ser Ala Ala
        35                  40                  45
Leu Leu Tyr Ala Ala Arg Ser Thr Pro Phe Ile Ala Asp Asn Val Leu
    50                  55                  60
Leu His Ala Leu Val Cys Ala Thr Tyr Ile Tyr Val Gln Gly Val Ile
65                  70                  75                  80
Phe Trp Gly Phe Phe Thr Val Gly His Asp Cys Gly His Ser Ala Phe
                85                  90                  95
Ser Arg Tyr His Ser Val Asn Phe Ile Ile Gly Cys Ile Met His Ser
            100                 105                 110
Ala Ile Leu Thr Pro Phe Glu Ser Trp Arg Val Thr His Arg His His
        115                 120                 125
His Lys Asn Thr Gly Asn Ile Asp Lys Asp Glu Ile Phe Tyr Pro His
    130                 135                 140
Arg Ser Val Lys Asp Leu Gln Asp Val Arg Gln Trp Val Tyr Thr Leu
145                 150                 155                 160
Gly Gly Ala Trp Phe Val Tyr Leu Lys Val Gly Tyr Ala Pro Arg Thr
                165                 170                 175
Met Ser His Phe Asp Pro Trp Asp Pro Leu Leu Leu Arg Arg Ala Ser
            180                 185                 190
Ala Val Ile Val Ser Leu Gly Val Trp Ala Ala Phe Phe Ala Ala Tyr
        195                 200                 205
Ala Tyr Leu Thr Tyr Ser Leu Gly Phe Ala Val Met Gly Leu Tyr Tyr
    210                 215                 220
Tyr Ala Pro Leu Phe Val Phe Ala Ser Phe Leu Val Ile Thr Thr Phe
225                 230                 235                 240
Leu His His Asn Asp Glu Ala Thr Pro Trp Tyr Gly Asp Ser Glu Trp
                245                 250                 255
Thr Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala
            260                 265                 270
Phe Val Asp Asn Leu Ser His His Ile Gly Thr His Gln Val His His
        275                 280                 285
Leu Phe Pro Ile Ile Pro His Tyr Lys Leu Asn Glu Ala Thr Lys His
    290                 295                 300
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Phe Ala Ala Ala Tyr Pro His Leu Val Arg Arg Asn Asp Glu Pro Ile
305                 310                 315                 320
Ile Thr Ala Phe Phe Lys Thr Ala His Leu Phe Val Asn Tyr Gly Ala
                325                 330                 335
Val Pro Glu Thr Ala Gln Ile Phe Thr Leu Lys Glu Ser Ala Ala Ala
            340                 345                 350
Ala Lys Ala Lys Ser Asp
        355
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<210> 27
<211> 1413
<212> DNA
<213> Saprolegnia diclina

<400> 27

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atcattatcc gcggcaaggt ctacgacgtg accgagtggg ccaacaagca ccccggcggc     180
cgcgagatgg tgctgctgca cgccggtcgc gaggccaccg acacgttcga ctcgtaccac     240
ccgttcagcg acaaggccga gtcgatcttg aacaagtatg agattggcac gttcacgggc     300
ccgtccgagt ttccgacctt caagccggac acgggcttct acaaggagtg ccgcaagcgc     360
gttggcgagt acttcaagaa gaacaacctc catccgcagg acggcttccc gggcctctgg     420
cgcatgatgg tcgtgtttgc ggtcgccggc ctcgccttgt acggcatgca cttttcgact     480
atctttgcgc tgcagctcgc ggccgcggcg ctctttggcg tctgccaggc gctgccgctg     540
ctccacgtca tgcacgactc gtcgcacgcg tcgtacacca acatgccgtt cttccattac     600
gtcgtcggcc gctttgccat ggactggttt gccggcggct cgatggtgtc atggctcaac     660
cagcacgtcg tgggccacca catctacacg aacgtcgcgg gctcggaccc ggatcttccg     720
gtcaacatgg acggcgacat ccgccgcatc gtgaaccgcc aggtgttcca gcccatgtac     780
gcattccagc acatctacct tccgccgctc tatggcgtgc ttggcctcaa gttccgcatc     840
caggacttca ccgacacgtt cggctcgcac acgaacggcc cgatccgcgt caacccgcac     900
gcgctctcga cgtggatggc catgatcagc tccaagtcgt tctgggcctt ctaccgcgtg     960
taccttccgc ttgccgtgct ccagatgccc atcaagacgt accttgcgat cttcttcctc    1020
gccgagtttg tcacgggctg gtacctcgcg ttcaacttcc aagtaagcca tgtctcgacc    1080
gagtgcggct acccatgcgg cgacgaggcc aagatggcgc tccaggacga gtgggcagtc    1140
tcgcaggtca agacgtcggt cgactacgcc catggctcgt ggatgacgac gttccttgcc    1200
ggcgcgctca actaccaggt cgtgcaccac ttgttcccca gcgtgtcgca gtaccactac    1260
ccggcgatcg cgcccatcat cgtcgacgtc tgcaaggagt acaacatcaa gtacgccatc    1320
ttgccggact ttacggcggc gttcgttgcc cacttgaagc acctccgcaa catgggccag    1380
cagggcatcg ccgccacgat ccacatgggc taa                                 1413
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<210> 28
<211> 819
<212> DNA
<213> Thraustochytrid sp.

<400> 28

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tggatggatg gcgccaagcc gtacgcactc accgatgggc tcccgatgat ggacgtgtcc     120
accatgctgg cattcgaggt gggatacatg gccatgctgc tcttcggcat cccgatcatg     180
aagcagatgg agaagccttt tgagctcaag accatcaagc tcttgcacaa cttgtttctc     240
ttcggacttt ccttgtacat gtgcgtggag accatccgcc aggctatcct cggaggctac     300
aaagtgtttg gaaacgacat ggagaagggc aacgagtctc atgctcaggg catgtctcgc     360
atcgtgtacg tgttctgcgt gtccaaggca tacgagttct tggataccgc catcatgatc     420
ctttgcaaga agttcaacca ggtttccttc ttgcatgtgt accaccatgc caccatttttt    480
gccatctggt gggctatcgc caagtacgct ccaggaggtg atgcgtactt ttcagtgatc     540
ctcaactctt tcgtgcacac cgtcatgtac gcatactact tcttctcctc ccaagggttc     600
gggttcgtga agccaatcaa gccgtacatc accacccttc agatgaccca gttcatggca     660
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atgcttgtgc agtccttgta cgactacctc ttcccatgcg actacccaca ggctcttgtg 720
cagcttcttg gagtgtacat gatcaccttg cttgccctct tcggcaactt ttttgtgcag 780
agctatctta aaaagccaaa aaagagcaag accaactaa 819

<210> 29
<211> 515
<212> PRT
<213> Saprolegnia diclina

<400> 29
Met Thr Val Gly Phe Asp Glu Thr Val Thr Met Asp Thr Val Arg Asn
1 5 10 15
His Asn Met Pro Asp Asp Ala Trp Cys Ala Ile His Gly Thr Val Tyr
20 25 30
Asp Ile Thr Lys Phe Ser Lys Val His Pro Gly Gly Asp Ile Ile Met
35 40 45
Leu Ala Ala Gly Lys Glu Ala Thr Ile Leu Phe Glu Thr Tyr His Ile
50 55 60
Lys Gly Val Pro Asp Ala Val Leu Arg Lys Tyr Lys Val Gly Lys Leu
65 70 75 80
Pro Gln Gly Lys Lys Gly Glu Thr Ser His Met Pro Thr Gly Leu Asp
85 90 95
Ser Ala Ser Tyr Tyr Ser Trp Asp Ser Glu Phe Tyr Arg Val Leu Arg
100 105 110
Glu Arg Val Ala Lys Lys Leu Ala Glu Pro Gly Leu Met Gln Arg Ala
115 120 125
Arg Met Glu Leu Trp Ala Lys Ala Ile Phe Leu Leu Ala Gly Phe Trp
130 135 140
Gly Ser Leu Tyr Ala Met Cys Val Leu Asp Pro His Gly Gly Ala Met
145 150 155 160
Val Ala Ala Val Thr Leu Gly Val Phe Ala Ala Phe Val Gly Thr Cys
165 170 175
Ile Gln His Asp Gly Ser His Gly Ala Phe Ser Lys Ser Arg Phe Met
180 185 190
Asn Lys Ala Ala Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Met
195 200 205
Thr Trp Glu Met Gln His Val Leu Gly His His Pro Tyr Thr Asn Leu
210 215 220
Ile Glu Met Glu Asn Gly Leu Ala Lys Val Lys Gly Ala Asp Val Asp
225 230 235 240
Pro Lys Lys Val Asp Gln Glu Ser Asp Pro Asp Val Phe Ser Thr Tyr
245 250 255
Pro Met Leu Arg Leu His Pro Trp His Arg Gln Arg Phe Tyr His Lys
260 265 270
Phe Gln His Leu Tyr Ala Pro Leu Ile Phe Gly Phe Met Thr Ile Asn
275 280 285
Lys Val Ile Ser Gln Asp Val Gly Val Val Leu Arg Lys Arg Leu Phe
290 295 300
Gln Ile Asp Ala Asn Cys Arg Tyr Gly Ser Pro Trp Asn Val Ala Arg
305 310 315 320
Phe Trp Ile Met Lys Leu Leu Thr Thr Leu Tyr Met Val Ala Leu Pro
325 330 335
Met Tyr Met Gln Gly Pro Ala Gln Gly Leu Lys Leu Phe Phe Met Ala
340 345 350
His Phe Thr Cys Gly Glu Val Leu Ala Thr Met Phe Ile Val Asn His
355 360 365
Ile Ile Glu Gly Val Ser Tyr Ala Ser Lys Asp Ala Val Lys Gly Val

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    370                 375                 380
Met Ala Pro Pro Arg Thr Val His Gly Val Thr Pro Met Gln Val Thr
385                 390                 395                 400
Gln Lys Ala Leu Ser Ala Ala Glu Ser Thr Lys Ser Asp Ala Asp Lys
                405                 410                 415
Thr Thr Met Ile Pro Leu Asn Asp Trp Ala Ala Val Gln Cys Gln Thr
            420                 425                 430
Ser Val Asn Trp Ala Val Gly Ser Trp Phe Trp Asn His Phe Ser Gly
        435                 440                 445
Gly Leu Asn His Gln Ile Glu His His Cys Phe Pro Gln Asn Pro His
    450                 455                 460
Thr Val Asn Val Tyr Ile Ser Gly Ile Val Lys Glu Thr Cys Glu Glu
465                 470                 475                 480
Tyr Gly Val Pro Tyr Gln Ala Glu Ile Ser Leu Phe Ser Ala Tyr Phe
                485                 490                 495
Lys Met Leu Ser His Leu Arg Thr Leu Gly Asn Glu Asp Leu Thr Ala
            500                 505                 510
Trp Ser Thr
        515
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<210> 30
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO967

<221> misc_feature
<222> (4)...(4)
<223> s = g or c at position 4

<221> misc_feature
<222> (12)...(12)
<223> s = g or c at position 12

<221> misc_feature
<222> (30)...(30)
<223> s = g or c at position 30

<221> misc_feature
<222> (31)...(31)
<223> k = g or t/u at position 31

<221> misc_feature
<222> (32)...(32)
<223> s = g or c at position 32

<400> 30
ccgsagttca csatcaagga gatccgcgas kscatcccgg cccactgctt c 51

<210> 31
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Reverse Primer RO968

<221> misc_feature
<222> (2)...(2)
<223> r = g or a at position 2

<221> misc_feature
<222> (3)...(3)
<223> s = g or c at position 3

<221> misc_feature
<222> (12)...(12)
<223> k = g or t/u at position 12

<221> misc_feature
<222> (17)...(17)
<223> w = a or t/u at position 17

<221> misc_feature
<222> (18)...(18)
<223> m = a or c at position 18

<221> misc_feature
<222> (19)...(19)
<223> s = g or c at position 19

<221> misc_feature
<222> (41)...(41)
<223> w = a or t/u at position 41

<221> misc_feature
<222> (42)...(42)
<223> r = g or a at position 42

<400> 31
grscttcttg akgtggwmsg tggcctcctc ggcgtggtag wrcggcat 48

<210> 32
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO964

<221> misc_feature
<222> (3)...(4)
<223> s = g or c at positions 3-4

<221> misc_feature
<222> (25)...(25)
<223> r = g or a at position 25

<221> misc_feature
<222> (36)...(36)
<223> s = g or c at position 36

<400> 32
ccsstctact gggcctgcca gggtrtcgtc ctcacsggtg tctgg 45

<210> 33
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO965

<221> misc_feature
<222> (3)...(4)
<223> s = g or c at positions 3-4

<221> misc_feature
<222> (16)...(16)
<223> r = g or a at position 16

<221> misc_feature
<222> (17)...(17)
<223> y = t/u or c at position 17

<221> misc_feature
<222> (18)...(18)
<223> s = g or c at position 18

<221> misc_feature
<222> (25)...(25)
<223> r = g or a at position 25

<221> misc_feature
<222> (31)...(31)
<223> k = g or t/u at position 31

<221> misc_feature
<222> (33)...(33)
<223> y = t/u or c at position 33

<221> misc_feature
<222> (36)...(36)
<223> s = g or c at position 36

<400> 33
ccsstctact ggatcrysca gggtrtcgtc kgyacsggtg tctgg 45

<210> 34
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO966

<221> misc_feature
<222> (19)...(19)
<223> s = g or c at position 19

<221> misc_feature
<222> (20)...(21)
<223> m = a or c at positions 20-21

<221> misc_feature
<222> (30)...(30)
<223> r = g or a at position 30

<400> 34
ggcgtggtag tgcggcatsm mcgagaagar gtggtgggcg acgtg 45

<210> 35
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO975

<400> 35
cacgtacctc cagcacacgg acacctacg 29

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO976

<400> 36
gatcgacagc gcgatccacc acattgc 27

<210> 37
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO977

<400> 37
caaatggtaa aagctagtgg cagcgctgc 29

<210> 38
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO978

<400> 38
agtacgtgcc ctggacgaac cagtagatg 29

<210> 39

<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1051

<400> 39
tcaacagaat tcatgtgcaa aggtcaagct ccttccaagg ccgacgtg 48

<210> 40
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1057

<400> 40
aaaagaaagc ttttactttt cctcgagctt gcgcttgtaa aacacaac 48

<210> 41
<211> 1182
<212> DNA
<213> Saprolegnia diclina

<400> 41
atgtgcaaag gtcaagctcc ttccaaggcc gacgtgttcc acgctgcggg gtaccgcccg 60
gtcgccggca cgcccgagcc gctgccgctg gagcccccga cgatcacgct caaggacctg 120
cgcgcggcga tcccggccca ctgctttgag cgcagcgctg ccactagctt ttaccatttg 180
gccaagaacc ttgcgatctg cgccggcgtg ttcgccgttg gcctcaagct cgcggctgcc 240
gacttgccgc tcgcggccaa gctggtcgcg tggcccatct actggttcgt ccagggcacg 300
tactttacgg gcatctgggt cattgcgcac gaatgcggcc accaggcgtt ctcggcgtcc 360
gagatcctca acgacacggt cggtatcatt cttcactcgc tcctctttgt gccgtaccac 420
agctggaaga tcacgcaccg ccgccaccac tccaacacgg gcagctgcga gaacgacgag 480
gtgtttacgc cgacgccgcg gtccgtcgtc gaggccaagc acgaccactc gctcctcgaa 540
gagagcccgc tctacaacct gtacggcatc gtcatgatgc ttctcgtggg ctggatgccg 600
ggctacctct tcttcaacgc gaccggcccg accaagtacg ctggcctcgc caagtcgcac 660
ttcaacccgt acgcagcctt tttcctccca aaggagcgcc tcagcatctg gtggagcgac 720
ctctgcttcc tcgcggcctt gtacggcttt ggctacggcg tctcggtctt cggcctcctc 780
gatgtcgccc gccactacat cgtgccgtac ctcatttgca acgcgtacct cgtgctcatc 840
acgtacctcc agcacacgga tacgtacgtg ccccacttcc gcggcgacga gtggaactgg 900
ctgcgcggcg cgctctgcac cgtcgaccgc tcgttcggcg cgtggatcga cagcgcgatc 960
caccacattg ccgacacgca cgtgacgcac cacattttct ccaagacgcc cttctaccac 1020
gcgatcgagg cgaccgacgc catcacgccc ctcctcggca agtactacct catcgacccg 1080
acgccgatcc cgctggcgct ctggcgctcg ttcacgcact gcaagtacgt cgaggacgac 1140
ggcaacgttg tgttttacaa gcgcaagctc gaggaaaagt aa 1182

<210> 42
<211> 393
<212> PRT
<213> Saprolegnia diclina

<400> 42
Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala
1 5 10 15
Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Leu Glu Pro

```
            20                  25                  30
Pro Thr Ile Thr Leu Lys Asp Leu Arg Ala Ala Ile Pro Ala His Cys
        35                  40                  45
Phe Glu Arg Ser Ala Ala Thr Ser Phe Tyr His Leu Ala Lys Asn Leu
    50                  55                  60
Ala Ile Cys Ala Gly Val Phe Ala Val Gly Leu Lys Leu Ala Ala Ala
65                  70                  75                  80
Asp Leu Pro Leu Ala Ala Lys Leu Val Ala Trp Pro Ile Tyr Trp Phe
                85                  90                  95
Val Gln Gly Thr Tyr Phe Thr Gly Ile Trp Val Ile Ala His Glu Cys
            100                 105                 110
Gly His Gln Ala Phe Ser Ala Ser Glu Ile Leu Asn Asp Thr Val Gly
        115                 120                 125
Ile Ile Leu His Ser Leu Leu Phe Val Pro Tyr His Ser Trp Lys Ile
    130                 135                 140
Thr His Arg Arg His His Ser Asn Thr Gly Ser Cys Glu Asn Asp Glu
145                 150                 155                 160
Val Phe Thr Pro Thr Pro Arg Ser Val Val Glu Ala Lys His Asp His
                165                 170                 175
Ser Leu Leu Glu Glu Ser Pro Leu Tyr Asn Leu Tyr Gly Ile Val Met
            180                 185                 190
Met Leu Leu Val Gly Trp Met Pro Gly Tyr Leu Phe Phe Asn Ala Thr
        195                 200                 205
Gly Pro Thr Lys Tyr Ala Gly Leu Ala Lys Ser His Phe Asn Pro Tyr
    210                 215                 220
Ala Ala Phe Phe Leu Pro Lys Glu Arg Leu Ser Ile Trp Trp Ser Asp
225                 230                 235                 240
Leu Cys Phe Leu Ala Ala Leu Tyr Gly Phe Gly Tyr Gly Val Ser Val
                245                 250                 255
Phe Gly Leu Leu Asp Val Ala Arg His Tyr Ile Val Pro Tyr Leu Ile
            260                 265                 270
Cys Asn Ala Tyr Leu Val Leu Ile Thr Tyr Leu Gln His Thr Asp Thr
        275                 280                 285
Tyr Val Pro His Phe Arg Gly Asp Glu Trp Asn Trp Leu Arg Gly Ala
    290                 295                 300
Leu Cys Thr Val Asp Arg Ser Phe Gly Ala Trp Ile Asp Ser Ala Ile
305                 310                 315                 320
His His Ile Ala Asp Thr His Val Thr His His Ile Phe Ser Lys Thr
                325                 330                 335
Pro Phe Tyr His Ala Ile Glu Ala Thr Asp Ala Ile Thr Pro Leu Leu
            340                 345                 350
Gly Lys Tyr Tyr Leu Ile Asp Pro Thr Pro Ile Pro Leu Ala Leu Trp
        355                 360                 365
Arg Ser Phe Thr His Cys Lys Tyr Val Glu Asp Asp Gly Asn Val Val
    370                 375                 380
Phe Tyr Lys Arg Lys Leu Glu Glu Lys
385                 390
```

<210> 43
<211> 393
<212> PRT
<213> Saprolegnia diclina

<400> 43

```
Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala
 1               5                  10                  15
Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Leu Glu Pro
```

```
            20                  25                  30
Pro Thr Ile Thr Leu Lys Asp Leu Arg Ala Ala Ile Pro Ala His Cys
        35                  40                  45
Phe Glu Arg Ser Ala Ala Thr Ser Phe Tyr His Leu Ala Lys Asn Leu
    50                  55                  60
Ala Ile Cys Ala Gly Val Phe Ala Val Gly Leu Lys Leu Ala Ala Ala
65                  70                  75                  80
Asp Leu Pro Leu Ala Ala Lys Leu Val Ala Trp Pro Ile Tyr Trp Phe
                85                  90                  95
Val Gln Gly Thr Tyr Phe Thr Gly Ile Trp Val Ile Ala His Glu Cys
            100                 105                 110
Gly His Gln Ala Phe Ser Ala Ser Glu Ile Leu Asn Asp Thr Val Gly
        115                 120                 125
Ile Ile Leu His Ser Leu Leu Phe Val Pro Tyr His Ser Trp Lys Ile
    130                 135                 140
Thr His Arg Arg His His Ser Asn Thr Gly Ser Cys Glu Asn Asp Glu
145                 150                 155                 160
Val Phe Thr Pro Thr Pro Arg Ser Val Val Glu Ala Lys His Asp His
                165                 170                 175
Ser Leu Leu Glu Glu Ser Pro Leu Tyr Asn Leu Tyr Gly Ile Val Met
            180                 185                 190
Met Leu Leu Val Gly Trp Met Pro Gly Tyr Leu Phe Phe Asn Ala Thr
        195                 200                 205
Gly Pro Thr Lys Tyr Ala Gly Leu Ala Lys Ser His Phe Asn Pro Tyr
    210                 215                 220
Ala Ala Phe Phe Leu Pro Lys Glu Arg Leu Ser Ile Trp Trp Ser Asp
225                 230                 235                 240
Leu Cys Phe Leu Ala Ala Leu Tyr Gly Phe Gly Tyr Gly Val Ser Val
                245                 250                 255
Phe Gly Leu Leu Asp Val Ala Arg His Tyr Ile Val Pro Tyr Leu Ile
            260                 265                 270
Cys Asn Ala Tyr Leu Val Leu Ile Thr Tyr Leu Gln His Thr Asp Thr
        275                 280                 285
Tyr Val Pro His Phe Arg Gly Asp Glu Trp Asn Trp Leu Arg Gly Ala
    290                 295                 300
Leu Cys Thr Val Asp Arg Ser Phe Gly Ala Trp Ile Asp Ser Ala Ile
305                 310                 315                 320
His His Ile Ala Asp Thr His Val Thr His His Ile Phe Ser Lys Thr
                325                 330                 335
Pro Phe Tyr His Ala Ile Glu Ala Thr Asp Ala Ile Thr Pro Leu Leu
            340                 345                 350
Gly Lys Tyr Tyr Leu Ile Asp Pro Thr Pro Ile Pro Leu Ala Leu Trp
        355                 360                 365
Arg Ser Phe Thr His Cys Lys Tyr Val Glu Asp Asp Gly Asn Val Val
    370                 375                 380
Phe Tyr Lys Arg Lys Leu Glu Glu Lys
385                 390
```

<210> 44
<211> 359
<212> PRT
<213> Synechocystis sp.

<220>
<221> VARIANT
<222> (315)...(315)
<223> Xaa = Unknown or Other at position 315

<221> VARIANT
<222> (331)...(331)
<223> Xaa = Unknown or Other at position 331

<400> 44

```
Tyr Phe Phe Leu Asp Val Gly Leu Ile Ala Gly Phe Tyr Ala Leu Ala
 1               5                  10                  15
Ala Tyr Leu Asp Ser Trp Phe Phe Tyr Pro Ile Phe Trp Leu Ile Gln
            20                  25                  30
Gly Thr Leu Phe Trp Ser Leu Phe Val Val Gly His Asp Cys Gly His
        35                  40                  45
Gly Ser Phe Ser Lys Ser Lys Thr Leu Asn Asn Trp Ile Gly His Leu
    50                  55                  60
Ser His Thr Pro Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His
65                  70                  75                  80
Arg Thr His His Ala Asn Thr Gly Asn Ile Asp Thr Asp Glu Ser Trp
                85                  90                  95
Tyr Pro Val Ser Glu Gln Lys Tyr Asn Gln Met Ala Trp Tyr Glu Lys
            100                 105                 110
Leu Leu Arg Phe Tyr Leu Pro Leu Ile Ala Tyr Pro Ile Tyr Leu Phe
        115                 120                 125
Arg Arg Ser Pro Asn Arg Gln Gly Ser His Phe Met Pro Gly Ser Pro
    130                 135                 140
Leu Phe Arg Pro Gly Glu Lys Ala Ala Val Leu Thr Ser Thr Phe Ala
145                 150                 155                 160
Leu Ala Ala Phe Val Gly Phe Leu Gly Phe Leu Thr Trp Gln Phe Gly
                165                 170                 175
Trp Leu Phe Leu Leu Lys Phe Tyr Val Ala Pro Tyr Leu Val Phe Val
            180                 185                 190
Val Trp Leu Asp Leu Val Thr Phe Leu His His Thr Glu Asp Asn Ile
        195                 200                 205
Pro Trp Tyr Arg Gly Asp Asp Trp Tyr Phe Leu Lys Gly Ala Leu Ser
    210                 215                 220
Thr Ile Asp Arg Asp Tyr Gly Phe Ile Asn Pro Ile His His Asp Ile
225                 230                 235                 240
Gly Thr His Val Ala His His Ile Phe Ser Asn Met Pro His Tyr Lys
                245                 250                 255
Leu Arg Arg Ala Thr Glu Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr
            260                 265                 270
Arg Tyr Ser Asp Glu Pro Ile Trp Gln Ala Phe Phe Lys Ser Tyr Trp
        275                 280                 285
Ala Cys His Phe Val Pro Asn Gln Gly Ser Gly Val Tyr Tyr Gln Ser
    290                 295                 300
Pro Ser Asn Gly Gly Tyr Gln Lys Lys Pro Xaa Leu Ile Leu Ile Glu
305                 310                 315                 320
Ser Asn Gln His Arg Glu Gly Arg Gln Tyr Xaa Met Val Leu Leu Pro
                325                 330                 335
Ser Asp Arg Leu Met Arg Ser Met Glu Glu Val Lys Gln Ser His Ser
            340                 345                 350
Lys Arg Ser Ala Leu Asn Gln
        355
```

<210> 45
<211> 358
<212> PRT
<213> Saprolegnia diclina

<400> 45
Met Thr Glu Asp Lys Thr Lys Val Glu Phe Pro Thr Leu Thr Glu Leu
1 5 10 15
Lys His Ser Ile Pro Asn Ala Cys Phe Glu Ser Asn Leu Gly Leu Ser
20 25 30
Leu Tyr Tyr Thr Ala Arg Ala Ile Phe Asn Ala Ser Ala Ser Ala Ala
35 40 45
Leu Leu Tyr Ala Ala Arg Ser Thr Pro Phe Ile Ala Asp Asn Val Leu
50 55 60
Leu His Ala Leu Val Cys Ala Thr Tyr Ile Tyr Val Gln Gly Val Ile
65 70 75 80
Phe Trp Gly Phe Phe Thr Val Gly His Asp Cys Gly His Ser Ala Phe
85 90 95
Ser Arg Tyr His Ser Val Asn Phe Ile Ile Gly Cys Ile Met His Ser
100 105 110
Ala Ile Leu Thr Pro Phe Glu Ser Trp Arg Val Thr His Arg His His
115 120 125
His Lys Asn Thr Gly Asn Ile Asp Lys Asp Glu Ile Phe Tyr Pro His
130 135 140
Arg Ser Val Lys Asp Leu Gln Asp Val Arg Gln Trp Val Tyr Thr Leu
145 150 155 160
Gly Gly Ala Trp Phe Val Tyr Leu Lys Val Gly Tyr Ala Pro Arg Thr
165 170 175
Met Ser His Phe Asp Pro Trp Asp Pro Leu Leu Leu Arg Arg Ala Ser
180 185 190
Ala Val Ile Val Ser Leu Gly Val Trp Ala Ala Phe Phe Ala Ala Tyr
195 200 205
Ala Tyr Leu Thr Tyr Ser Leu Gly Phe Ala Val Met Gly Leu Tyr Tyr
210 215 220
Tyr Ala Pro Leu Phe Val Phe Ala Ser Phe Leu Val Ile Thr Thr Phe
225 230 235 240
Leu His His Asn Asp Glu Ala Thr Pro Trp Tyr Gly Asp Ser Glu Trp
245 250 255
Thr Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala
260 265 270
Phe Val Asp Asn Leu Ser His His Ile Gly Thr His Gln Val His His
275 280 285
Leu Phe Pro Ile Ile Pro His Tyr Lys Leu Asn Glu Ala Thr Lys His
290 295 300
Phe Ala Ala Ala Tyr Pro His Leu Val Arg Arg Asn Asp Glu Pro Ile
305 310 315 320
Ile Thr Ala Phe Phe Lys Thr Ala His Leu Phe Val Asn Tyr Gly Ala
325 330 335
Val Pro Glu Thr Ala Gln Ile Phe Thr Leu Lys Glu Ser Ala Ala Ala
340 345 350
Ala Lys Ala Lys Ser Asp
355

<210> 46
<211> 409
<212> PRT
<213> Caenorhabitis elegans

<220>
<221> VARIANT
<222> (389)...(389)

<223> Xaa = Unknown or Other at position 389

<400> 46

```
Val Thr Gly Gly Asp Val Leu Val Asp Ala Arg Ala Ser Leu Glu Glu
 1               5                  10                  15
Lys Glu Ala Pro Arg Asp Val Asn Ala Asn Thr Lys Gln Ala Thr Thr
            20                  25                  30
Glu Glu Pro Arg Ile Gln Leu Pro Thr Val Asp Ala Phe Arg Arg Ala
        35                  40                  45
Ile Pro Ala His Cys Phe Glu Arg Asp Leu Val Lys Ser Ile Arg Tyr
    50                  55                  60
Leu Val Gln Asp Phe Ala Ala Leu Thr Ile Leu Tyr Phe Ala Leu Pro
65                  70                  75                  80
Ala Phe Glu Tyr Phe Gly Leu Phe Gly Tyr Leu Val Trp Asn Ile Phe
                85                  90                  95
Met Gly Val Phe Gly Phe Ala Leu Phe Val Val Gly His Asp Cys Leu
            100                 105                 110
His Gly Ser Phe Ser Asp Asn Gln Asn Leu Asn Asp Phe Ile Gly His
        115                 120                 125
Ile Ala Phe Ser Pro Leu Phe Ser Pro Tyr Phe Pro Trp Gln Lys Ser
    130                 135                 140
His Lys Leu His His Ala Phe Thr Asn His Ile Asp Lys Asp His Gly
145                 150                 155                 160
His Val Trp Ile Gln Asp Lys Asp Trp Glu Ala Met Pro Ser Trp Lys
                165                 170                 175
Arg Trp Phe Asn Pro Ile Pro Phe Ser Gly Trp Leu Lys Trp Phe Pro
            180                 185                 190
Val Tyr Thr Leu Phe Gly Phe Cys Asp Gly Ser His Phe Trp Pro Tyr
        195                 200                 205
Ser Ser Leu Phe Val Arg Asn Ser Asp Arg Val Gln Cys Val Ile Ser
    210                 215                 220
Gly Ile Cys Cys Cys Val Cys Ala Tyr Ile Ala Leu Thr Ile Ala Gly
225                 230                 235                 240
Ser Tyr Ser Asn Trp Phe Trp Tyr Tyr Trp Val Pro Leu Ser Phe Phe
                245                 250                 255
Gly Leu Met Leu Val Ile Val Thr Tyr Leu Gln His Val Asp Asp Val
            260                 265                 270
Ala Glu Val Tyr Glu Ala Asp Glu Trp Ser Phe Val Arg Gly Gln Thr
        275                 280                 285
Gln Thr Ile Asp Arg Tyr Tyr Gly Leu Gly Leu Asp Thr Thr Met His
    290                 295                 300
His Ile Thr Asp Gly His Val Ala His His Phe Phe Asn Lys Ile Pro
305                 310                 315                 320
His Tyr His Leu Ile Glu Ala Thr Glu Gly Val Lys Lys Val Leu Glu
                325                 330                 335
Pro Leu Ser Asp Thr Gln Tyr Gly Tyr Lys Ser Gln Val Asn Tyr Asp
            340                 345                 350
Phe Phe Ala Arg Phe Leu Trp Phe Asn Tyr Lys Leu Asp Tyr Leu Val
        355                 360                 365
His Lys Thr Ala Gly Ile Met Gln Phe Arg Thr Thr Leu Glu Glu Lys
    370                 375                 380
Ala Lys Ala Lys Xaa Lys Asn Ile Pro Cys Arg Ser Arg Val Gln Gln
385                 390                 395                 400
Gln Leu Leu Arg Phe His Arg Phe Cys
                405
```

<210> 47

<211> 333
<212> PRT
<213> Saprolegnia diclina

<400> 47
Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala
1 5 10 15
Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Leu Glu Pro
20 25 30
Pro Thr Ile Thr Leu Lys Asp Leu Arg Ala Ala Ile Pro Ala His Cys
35 40 45
Phe Glu Arg Ser Ala Ala Thr Ser Phe Tyr His Leu Ala Lys Asn Leu
50 55 60
Ala Ile Cys Ala Gly Val Phe Ala Val Gly Leu Lys Leu Ala Ala Ala
65 70 75 80
Asp Leu Pro Leu Ala Ala Lys Leu Val Ala Trp Pro Ile Tyr Trp Phe
85 90 95
Val Gln Gly Thr Tyr Phe Thr Gly Ile Trp Val Ile Ala His Glu Cys
100 105 110
Gly His Gln Ala Phe Ser Ala Ser Glu Ile Leu Asn Asp Thr Val Gly
115 120 125
Ile Ile Leu His Ser Leu Leu Phe Val Pro Tyr His Ser Trp Lys Ile
130 135 140
Thr His Arg Arg His His Ser Asn Thr Gly Ser Cys Glu Asn Asp Glu
145 150 155 160
Val Phe Thr Pro Thr Pro Arg Ser Val Val Glu Ala Lys His Asp His
165 170 175
Ser Leu Leu Glu Glu Ser Pro Leu Tyr Asn Leu Tyr Gly Ile Val Met
180 185 190
Met Leu Leu Val Gly Trp Met Pro Gly Tyr Leu Phe Phe Asn Ala Thr
195 200 205
Gly Pro Thr Lys Tyr Ala Gly Leu Ala Lys Ser His Phe Asn Pro Tyr
210 215 220
Ala Ala Phe Phe Leu Pro Lys Glu Arg Leu Ser Ile Trp Trp Ser Asp
225 230 235 240
Leu Cys Phe Leu Ala Ala Leu Tyr Gly Phe Gly Tyr Gly Val Ser Val
245 250 255
Phe Gly Leu Leu Asp Val Ala Arg His Tyr Ile Val Pro Tyr Leu Ile
260 265 270
Cys Asn Ala Tyr Leu Val Leu Ile Thr Tyr Leu Gln His Thr Asp Thr
275 280 285
Thr Pro Leu Leu Gly Lys Tyr Tyr Leu Ile Asp Pro Thr Pro Ile Pro
290 295 300
Leu Ala Leu Trp Arg Ser Phe Thr His Cys Lys Tyr Val Glu Asp Asp
305 310 315 320
Gly Asn Val Val Phe Tyr Lys Arg Lys Leu Glu Glu Lys
325 330

<210> 48
<211> 412
<212> PRT
<213> Gossypium hirsutum

<220>
<221> VARIANT
<222> (9)...(9)
<223> Xaa = Unknown or Other at position 9

<221> VARIANT
<222> (403)...(403)
<223> Xaa = Unknown or Other at position 403

<400> 48

```
Leu Arg Val Ser Ser Thr Trp Arg Xaa Thr Ala Phe Phe Lys Ala Ser
 1               5                  10                  15
Lys Met Gly Ala Gly Gly Arg Met Pro Ile Asp Gly Ile Lys Glu Glu
            20                  25                  30
Asn Arg Gly Ser Val Asn Arg Val Pro Ile Glu Lys Pro Pro Phe Thr
        35                  40                  45
Leu Gly Gln Ile Lys Gln Ala Ile Pro Pro His Cys Phe Arg Arg Ser
    50                  55                  60
Leu Leu Arg Ser Phe Ser Tyr Val Val His Asp Leu Cys Leu Ala Ser
65                  70                  75                  80
Phe Phe Tyr Tyr Ile Ala Thr Ser Tyr Phe His Phe Leu Pro Gln Pro
                85                  90                  95
Phe Ser Tyr Ile Ala Trp Pro Val Tyr Trp Val Leu Gln Gly Cys Ile
            100                 105                 110
Leu Thr Gly Val Trp Val Ile Ala His Glu Trp Gly His His Ala Phe
        115                 120                 125
Arg Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Leu Ile Leu His Ser
    130                 135                 140
Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Ile Ser His Arg Arg His
145                 150                 155                 160
His Ser Asn Thr Gly Ser Met Glu Arg Asp Glu Val Phe Val Pro Lys
                165                 170                 175
Pro Lys Ser Lys Leu Ser Cys Phe Ala Lys Tyr Leu Asn Asn Pro Pro
            180                 185                 190
Gly Arg Val Leu Ser Leu Val Val Thr Leu Thr Leu Gly Trp Pro Met
        195                 200                 205
Tyr Leu Ala Phe Asn Val Ser Gly Arg Tyr Tyr Asp Arg Leu Ala Ser
    210                 215                 220
His Tyr Asn Pro Tyr Gly Pro Ile Tyr Ser Asp Arg Glu Arg Leu Gln
225                 230                 235                 240
Val Tyr Ile Ser Asp Thr Gly Ile Phe Ala Val Ile Tyr Val Leu Tyr
                245                 250                 255
Lys Ile Ala Ala Thr Lys Gly Leu Ala Trp Leu Leu Cys Thr Tyr Gly
            260                 265                 270
Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
        275                 280                 285
Gln His Thr His Ser Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
    290                 295                 300
Trp Leu Arg Gly Ala Leu Ser Thr Met Asp Arg Asp Phe Gly Val Leu
305                 310                 315                 320
Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
                325                 330                 335
Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
            340                 345                 350
Lys Pro Ile Leu Gly Lys Tyr Tyr Pro Phe Asp Gly Thr Pro Ile Tyr
        355                 360                 365
Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro Asp
    370                 375                 380
Val Gly Gly Gly Gly Gly Gly Ser Lys Gly Val Phe Trp Tyr Arg Asn
385                 390                 395                 400
Lys Phe Xaa Arg Pro Thr Asn Cys Leu Ile Ala Gly
```

405 410

<210> 49
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 1 from Example 3

<400> 49
Thr Arg Ala Ala Ile Pro Lys His Cys Trp Val Lys
1 5 10

<210> 50
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 2 from Example 3

<400> 50
Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser
1 5 10 15

<210> 51
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 3 from Example 3

<400> 51
Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn
1 5 10 15

<210> 52
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 4 from Example 3

<221> VARIANT
<222> (5)...(5)
<223> Xaa = D or H at position 5

<221> VARIANT
<222> (7)...(7)
<223> Xaa = D or Y at position 7

<400> 52
Gly Ser His Phe Xaa Pro Xaa Ser Asp Leu Phe Val
1 5 10

<210> 53
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 5 from Example 3

<221> VARIANT
<222> (3)...(3)
<223> Xaa = Y or F at position 3

<221> VARIANT
<222> (4)...(4)
<223> Xaa = L or V at position 4

<221> VARIANT
<222> (11)...(11)
<223> Xaa = L or I at position 11

<400> 53
Trp Ser Xaa Xaa Arg Gly Gly Leu Thr Thr Xaa Asp Arg
 1   5   10

<210> 54
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 6 from Example 3

<400> 54
His His Asp Ile Gly Thr His Val Ile His His Leu Phe Pro Gln
 1   5   10   15

<210> 55
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 7 from Example 3

<221> VARIANT
<222> (2)...(2)
<223> Xaa = L or F at position 2

<221> VARIANT
<222> (5)...(5)
<223> Xaa = Q or K at position 5

<221> VARIANT
<222> (12)...(12)
<223> Xaa = V or I at position 12

<400> 55
His Xaa Phe Pro Xaa Ile Pro His Tyr His Leu Xaa Glu Ala Thr
1 5 10 15

<210> 56
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 8 from Example 3

<221> VARIANT
<222> (3)...(3)
<223> Xaa = A or I at position 3

<221> VARIANT
<222> (6)...(6)
<223> Xaa = L or F at position 6

<400> 56
His Val Xaa His His Xaa Phe Pro Gln Ile Pro His Tyr His Leu
1 5 10 15

<210> 57
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 1 from Example 7

<221> VARIANT
<222> (2)...(2)
<223> Xaa = N or E at position 2

<221> VARIANT
<222> (10)...(10)
<223> Xaa = D or E at position 10

<221> VARIANT
<222> (11)...(11)
<223> Xaa = A or C at position 11

<400> 57
Pro Xaa Phe Thr Ile Lys Glu Ile Arg Xaa Xaa Ile Pro Ala His Cys
1 5 10 15
Phe

<210> 58
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 2 from Example 7

<221> VARIANT
<222> (3)...(3)
<223> Xaa = H or F at position 3

<221> VARIANT
<222> (11)...(11)
<223> Xaa = V or Y at position 11

<221> VARIANT
<222> (13)...(13)
<223> Xaa = I or L at position 13

<221> VARIANT
<222> (16)...(16)
<223> Xaa = A or L at position 16

<400> 58
Met Pro Xaa Tyr His Ala Glu Glu Ala Thr Xaa His Xaa Lys Lys Xaa
1 5 10 15

<210> 59
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 3 from Example 7

<221> VARIANT
<222> (2)...(2)
<223> Xaa = L or V at position 2

<221> VARIANT
<222> (5)...(5)
<223> Xaa = A or I at position 5

<221> VARIANT
<222> (6)...(6)
<223> Xaa = C or M or A at position 6

<221> VARIANT
<222> (9)...(9)
<223> Xaa = V or I at position 9

<221> VARIANT
<222> (11)...(11)
<223> Xaa = L or G or C at position 11

<400> 59
Pro Xaa Tyr Trp Xaa Xaa Gln Gly Xaa Val Xaa Thr Gly Val Trp
1 5 10 15

<210> 60
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 4 from Example 7

<221> VARIANT
<222> (6)...(6)
<223> Xaa = L or F at position 6

<221> VARIANT
<222> (9)...(9)
<223> Xaa = T or Q at position 9

<400> 60
His Val Ala His His Xaa Phe Ser Xaa Met Pro His Tyr His Ala
1 5 10 15